

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/527,646
Source: PGT/10
Date Processed by STIC: 3/25/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 03/25/2005

PATENT APPLICATION: US/10/527,646

TIME: 11:08:30

Input Set : A:\2958-131.txt

Output Set: N:\CRF4\03252005\J527646.raw

3 <110> APPLICANT: Nitsch, Robert
 4 Ninnemann, Olaf
 5 Braeuer, Anja
 6 Savaskan, Nicolai
 8 <120> TITLE OF INVENTION: Lipid Phosphate Phosphatases and Uses Therefor for Treating
 9 Neuronal Diseases
 11 <130> FILE REFERENCE: 2958-131
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/527,646
 C--> 13 <141> CURRENT FILING DATE: 2005-03-14
 13 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/010228
 14 <151> PRIOR FILING DATE: 2003-09-15
 16 <150> PRIOR APPLICATION NUMBER: 03002993.8
 17 <151> PRIOR FILING DATE: 2003-02-11
 19 <150> PRIOR APPLICATION NUMBER: 02020679.3
 20 <151> PRIOR FILING DATE: 2002-09-13
 22 <160> NUMBER OF SEQ ID NOS: 38
 24 <170> SOFTWARE: PatentIn version 3.3
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 763
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Homo sapiens
 31 <400> SEQUENCE: 1
 33 Met Gln Arg Ala Gly Ser Ser Gly Gly Arg Gly Glu Cys Asp Ile Ser
 34 1 5 10 15
 37 Gly Ala Gly Arg Leu Gly Leu Glu Glu Ala Ala Arg Leu Ser Cys Ala
 38 20 25 30
 41 Val His Thr Ser Pro Gly Gly Gly Arg Arg Pro Gly Gln Ala Ala Gly
 42 35 40 45
 45 Met Ser Ala Lys Glu Arg Pro Lys Gly Lys Val Ile Lys Asp Ser Val
 46 50 55 60
 49 Thr Leu Leu Pro Cys Phe Tyr Phe Val Glu Leu Pro Ile Leu Ala Ser
 50 65 70 75 80
 53 Ser Val Val Ser Leu Tyr Phe Leu Glu Leu Thr Asp Val Phe Lys Pro
 54 85 90 95
 57 Val His Ser Gly Phe Ser Cys Tyr Asp Arg Ser Leu Ser Met Pro Tyr
 58 100 105 110
 61 Ile Glu Pro Thr Gln Glu Ala Ile Pro Phe Leu Met Leu Leu Ser Leu
 62 115 120 125
 65 Ala Phe Ala Gly Pro Ala Ile Thr Ile Met Val Gly Glu Gly Ile Leu
 66 130 135 140
 69 Tyr Cys Cys Leu Ser Lys Arg Arg Asn Gly Val Gly Leu Glu Pro Asn
 70 145 150 155 160
 73 Ile Asn Ala Gly Gly Cys Asn Phe Asn Ser Phe Leu Arg Arg Ala Val

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74          165          170          175
77 Arg Phe Val Gly Val His Val Phe Gly Leu Cys Ser Thr Ala Leu Ile
78          180          185          190
81 Thr Asp Ile Ile Gln Leu Ser Thr Gly Tyr Gln Ala Pro Tyr Phe Leu
82          195          200          205
85 Thr Val Cys Lys Pro Asn Tyr Thr Ser Leu Asn Val Ser Cys Lys Glu
86          210          215          220
89 Asn Ser Tyr Ile Val Glu Asp Ile Cys Ser Gly Ser Asp Leu Thr Val
90 225          230          235          240
93 Ile Asn Ser Gly Arg Lys Ser Phe Pro Ser Gln His Ala Thr Leu Ala
94          245          250          255
97 Ala Phe Ala Ala Val Tyr Val Ser Met Tyr Phe Asn Ser Thr Leu Thr
98          260          265          270
101 Asp Ser Ser Lys Leu Leu Lys Pro Leu Leu Val Phe Thr Phe Ile Ile
102          275          280          285
105 Cys Gly Ile Ile Cys Gly Leu Thr Arg Ile Thr Gln Tyr Lys Asn His
106          290          295          300
109 Pro Val Asp Val Tyr Cys Gly Phe Leu Ile Gly Gly Gly Ile Ala Leu
110 305          310          315          320
113 Tyr Leu Gly Leu Tyr Ala Val Gly Asn Phe Leu Pro Ser Asp Glu Ser
114          325          330          335
117 Met Phe Gln His Arg Asp Ala Leu Arg Ser Leu Thr Asp Leu Asn Gln
118          340          345          350
121 Asp Pro Asn Arg Leu Leu Ser Ala Lys Asn Gly Ser Ser Ser Asp Gly
122          355          360          365
125 Ile Ala His Thr Glu Gly Ile Leu Asn Arg Asn His Arg Asp Ala Ser
126          370          375          380
129 Ser Leu Thr Asn Leu Lys Arg Ala Asn Ala Asp Val Glu Ile Ile Thr
130 385          390          395          400
133 Pro Arg Ser Pro Met Gly Lys Glu Asn Met Val Thr Phe Ser Asn Thr
134          405          410          415
137 Leu Pro Arg Ala Asn Thr Pro Ser Val Glu Asp Pro Val Arg Arg Asn
138          420          425          430
141 Ala Ser Ile His Ala Ser Met Asp Ser Ala Arg Ser Lys Gln Leu Leu
142          435          440          445
145 Thr Gln Trp Lys Asn Lys Asn Glu Ser Arg Lys Leu Ser Leu Gln Val
146          450          455          460
149 Ile Glu Pro Glu Pro Gly Gln Ser Pro Pro Arg Ser Ile Glu Met Arg
150 465          470          475          480
153 Ser Ser Ser Glu Pro Ser Arg Val Gly Val Asn Gly Asp His His Gly
154          485          490          495
157 Pro Gly Asn Gln Tyr Leu Lys Ile Gln Pro Gly Ala Val Pro Gly Cys
158          500          505          510
161 Asn Asn Ser Met Pro Gly Gly Pro Arg Val Ser Ile Gln Ser Arg Pro
162          515          520          525
165 Gly Ser Ser Gln Leu Val His Ile Pro Glu Glu Thr Gln Glu Asn Ile
166          530          535          540
169 Ser Thr Ser Pro Lys Ser Ser Ala Arg Ala Lys Trp Leu Lys Ala
170 545          550          555          560

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173 Ala Glu Lys Thr Val Ala Cys Asn Arg Ser Asn Ser Gln Pro Arg Ile
174                               565                               570                               575
177 Met Gln Val Ile Ala Met Ser Lys Gln Gln Gly Val Leu Gln Ser Ser
178                               580                               585                               590
181 Pro Lys Asn Thr Glu Gly Ser Thr Val Ser Cys Thr Gly Ser Ile Arg
182                               595                               600                               605
185 Tyr Lys Thr Leu Thr Asp His Glu Pro Ser Gly Ile Val Arg Val Glu
186                               610                               615                               620
189 Ala His Pro Glu Asn Asn Arg Pro Ile Ile Gln Ile Pro Ser Thr Glu
190 625                               630                               635                               640
193 Gly Glu Gly Ser Gly Ser Trp Lys Trp Lys Ala Pro Glu Lys Gly Ser
194                               645                               650                               655
197 Leu Arg Gln Thr Tyr Glu Leu Asn Asp Leu Asn Arg Asp Ser Glu Ser
198                               660                               665                               670
201 Cys Glu Ser Leu Lys Asp Ser Phe Gly Ser Gly Asp Arg Lys Arg Ser
202                               675                               680                               685
205 Asn Ile Asp Ser Asn Glu His His His His Gly Ile Thr Thr Ile Arg
206                               690                               695                               700
209 Val Thr Pro Val Glu Gly Ser Glu Ile Gly Ser Glu Thr Leu Ser Ile
210 705                               710                               715                               720
213 Ser Ser Ser Arg Asp Ser Thr Leu Arg Arg Lys Gly Asn Ile Ile Leu
214                               725                               730                               735
217 Ile Pro Glu Arg Ser Asn Ser Pro Glu Asn Thr Arg Asn Ile Phe Tyr
218                               740                               745                               750
221 Lys Gly Thr Ser Pro Thr Arg Ala Tyr Lys Asp
222                               755                               760
225 <210> SEQ ID NO: 2
226 <211> LENGTH: 746
227 <212> TYPE: PRT
228 <213> ORGANISM: Homo sapiens
230 <400> SEQUENCE: 2
232 Met Ile Ser Thr Lys Glu Lys Asn Lys Ile Pro Lys Asp Ser Met Thr
233 1                               5                               10                               15
236 Leu Leu Pro Cys Phe Tyr Phe Val Glu Leu Pro Ile Val Ala Ser Ser
237                               20                               25                               30
240 Ile Val Ser Leu Tyr Phe Leu Glu Leu Thr Asp Leu Phe Lys Pro Ala
241                               35                               40                               45
244 Lys Val Gly Phe Gln Cys Tyr Asp Arg Thr Leu Ser Met Pro Tyr Val
245                               50                               55                               60
248 Glu Thr Asn Glu Glu Leu Ile Pro Leu Leu Met Leu Leu Ser Leu Ala
249 65                               70                               75                               80
252 Phe Ala Ala Pro Ala Ala Ser Ile Met Val Ala Glu Gly Met Leu Tyr
253                               85                               90                               95
256 Cys Leu Gln Ser Arg Leu Trp Gly Arg Ala Gly Gly Pro Ala Gly Ala
257                               100                              105                              110
260 Glu Gly Ser Ile Asn Ala Gly Gly Cys Asn Phe Asn Ser Phe Leu Arg
261                               115                              120                              125
264 Arg Thr Val Arg Phe Val Gly Val His Val Phe Gly Leu Cys Ala Thr
265                               130                              135                              140

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268 Ala Leu Val Thr Asp Val Ile Gln Leu Ala Thr Gly Tyr His Thr Pro
269 145 150 155 160
272 Phe Phe Leu Thr Val Cys Lys Pro Asn Tyr Thr Leu Leu Gly Thr Ser
273 165 170 175
276 Cys Glu Val Asn Pro Tyr Ile Thr Gln Asp Ile Cys Ser Gly His Asp
277 180 185 190
280 Ile His Ala Ile Leu Ser Ala Arg Lys Thr Phe Pro Ser Gln His Ala
281 195 200 205
284 Thr Leu Ser Ala Phe Ala Ala Val Tyr Val Ser Val Ser Pro Ala Pro
285 210 215 220
288 His Cys Pro Ser Gln Ala Leu Leu Leu Thr Arg Gly Glu Pro Ser Leu
289 225 230 235 240
292 Thr Pro Thr Pro Met Pro Gln Met Tyr Phe Asn Ser Val Ile Ser Asp
293 245 250 255
296 Thr Thr Lys Leu Leu Lys Pro Ile Leu Val Phe Ala Phe Ala Ile Ala
297 260 265 270
300 Ala Gly Val Cys Gly Leu Thr Gln Ile Thr Gln Tyr Arg Ser His Pro
301 275 280 285
304 Val Asp Val Tyr Ala Gly Phe Leu Ile Gly Ala Gly Ile Ala Ala Tyr
305 290 295 300
308 Leu Ala Cys His Ala Val Gly Asn Phe Gln Ala Pro Pro Ala Glu Lys
309 305 310 315 320
312 Pro Ala Ala Pro Ala Pro Ala Lys Asp Ala Leu Arg Ala Leu Thr Gln
313 325 330 335
316 Arg Gly His Asp Ser Val Tyr Gln Gln Asn Lys Ser Val Ser Thr Asp
317 340 345 350
320 Glu Leu Gly Pro Pro Gly Arg Leu Glu Gly Ala Pro Arg Pro Val Ala
321 355 360 365
324 Arg Glu Lys Thr Ser Leu Gly Ser Leu Lys Arg Ala Ser Val Asp Val
325 370 375 380
328 Asp Leu Leu Ala Pro Arg Ser Pro Met Ala Lys Glu Asn Met Val Thr
329 385 390 395 400
332 Phe Ser His Thr Leu Pro Arg Ala Ser Ala Pro Ser Leu Asp Asp Pro
333 405 410 415
336 Ala Arg Arg His Met Thr Ile His Val Pro Leu Asp Ala Ser Arg Ser
337 420 425 430
340 Lys Gln Leu Ile Ser Glu Trp Lys Gln Lys Ser Leu Glu Gly Arg Gly
341 435 440 445
344 Leu Gly Leu Pro Asp Asp Ala Ser Pro Gly His Leu Arg Ala Pro Ala
345 450 455 460
348 Glu Pro Met Ala Glu Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu Glu
349 465 470 475 480
352 Glu Glu Glu Glu Glu Glu Glu Asp Glu Gly Pro Ala Pro Pro Ser Leu
353 485 490 495
356 Tyr Pro Thr Val Gln Ala Arg Pro Gly Leu Gly Pro Arg Val Ile Leu
357 500 505 510
360 Pro Pro Arg Ala Gly Pro Pro Pro Leu Val His Ile Pro Glu Glu Gly
361 515 520 525
364 Ala Gln Thr Gly Ala Gly Leu Ser Pro Lys Ser Gly Ala Gly Val Arg

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```

365      530      535      540
368 Ala Lys Trp Leu Met Met Ala Glu Lys Ser Gly Ala Ala Val Ala Asn
369 545      550      555      560
372 Pro Pro Arg Leu Leu Gln Val Ile Ala Met Ser Lys Ala Pro Gly Ala
373      565      570      575
376 Pro Gly Pro Lys Ala Ala Glu Thr Ala Ser Ser Ser Ser Ala Ser Ser
377      580      585      590
380 Asp Ser Ser Gln Tyr Arg Ser Pro Ser Asp Arg Asp Ser Ala Ser Ile
381      595      600      605
384 Val Thr Ile Asp Ala His Ala Pro His His Pro Val Val His Leu Ser
385      610      615      620
388 Ala Gly Gly Ala Pro Trp Glu Trp Lys Ala Ala Gly Gly Gly Ala Lys
389 625      630      635      640
392 Ala Glu Ala Asp Gly Gly Tyr Glu Leu Gly Asp Leu Ala Arg Gly Phe
393      645      650      655
396 Arg Gly Gly Ala Lys Pro Pro Gly Val Ser Pro Gly Ser Ser Val Ser
397      660      665      670
400 Asp Val Asp Gln Glu Glu Pro Arg Phe Gly Ala Val Ala Thr Val Asn
401      675      680      685
404 Leu Ala Thr Gly Glu Gly Leu Pro Pro Leu Gly Ala Ala Asp Gly Ala
405      690      695      700
408 Leu Gly Pro Gly Ser Arg Glu Ser Thr Leu Arg Arg His Ala Gly Gly
409 705      710      715      720
412 Leu Gly Leu Ala Glu Arg Glu Ala Glu Ala Glu Gly Tyr Phe
413      725      730      735
416 Arg Lys Met Gln Ala Arg Arg Phe Pro Asp
417      740      745
420 <210> SEQ ID NO: 3
421 <211> LENGTH: 325
422 <212> TYPE: PRT
423 <213> ORGANISM: Homo sapiens
425 <400> SEQUENCE: 3
427 Met Ala Val Gly Asn Asn Thr Gln Arg Ser Tyr Ser Ile Ile Pro Cys
428 1      5      10      15
431 Phe Ile Phe Val Glu Leu Val Ile Met Ala Gly Thr Val Leu Leu Ala
432      20      25      30
435 Tyr Tyr Phe Glu Cys Thr Asp Thr Phe Gln Val His Ile Gln Gly Phe
436      35      40      45
439 Phe Cys Gln Asp Gly Asp Leu Met Lys Pro Tyr Pro Gly Thr Glu Glu
440      50      55      60
443 Glu Ser Phe Ile Thr Pro Leu Val Leu Tyr Cys Val Leu Ala Ala Thr
444 65      70      75      80
447 Pro Thr Ala Ile Ile Phe Ile Gly Glu Ile Ser Met Tyr Phe Ile Lys
448      85      90      95
451 Ser Thr Arg Glu Ser Leu Ile Ala Gln Glu Lys Thr Ile Leu Thr Gly
452      100      105      110
455 Glu Cys Cys Tyr Leu Asn Pro Leu Leu Arg Arg Ile Ile Arg Phe Thr
456      115      120      125
459 Gly Val Phe Ala Phe Gly Leu Phe Ala Thr Asp Ile Phe Val Asn Ala

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/527,646

DATE: 03/25/2005
TIME: 11:08:31

Input Set : A:\2958-131.txt
Output Set: N:\CRF4\03252005\J527646.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; N Pos. 460

Seq#:21; N Pos. 1137,2899,2917,2918,2919,2921,2922,2923,2924,2929

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/527,646

DATE: 03/25/2005

TIME: 11:08:31

Input Set : A:\2958-131.txt

Output Set: N:\CRF4\03252005\J527646.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2196 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:420
L:2774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:1080
M:341 Repeated in SeqNo=21